



Revised March 29, 2004- 39754-0611 US.txt

SEQUENCE LISTING

<110> WALKER, Ameae M.

<120> PROLACTIN ANTAGONISTS AND USES THEREOF

<130> 39754-0611-1CP1CP

<140> US 09/065,330

<141> 1998-04-23

<150> PCT/US97/01435

<151> 1997-01-30

<150> US 08/594,809

<151> 1996-01-31

<160> 6

<170> FastSEQ for windows Version 4.0

<210> 1

<211> 832

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (622)...(624)

<223> This is the codon for the substituted amino acids
of the mutated sequence.

<400> 1

aacatgaaca	tcaaaggatc	gccatggaaa	gggtccctcc	tgctgctgct	ggtgtcaaac	60
ctgctgctgt	gccagagcgt	ggcccccttg	cccatactgtc	ccggcggggc	tgcccgatgc	120
caggtgaccc	ttcgagacct	gtttgaccgc	gccgtcgctc	tgtcccacta	catccataac	180
ctctcctcag	aaatgttcag	cgaattcgat	aaacggtata	cccatggccg	gggggttcatt	240
accaaggcca	tcaacagctg	ccacacttct	tcccttgcca	ccccgaaga	caaggagcaa	300
gccaacaga	tgaatcaaaa	agactttctg	agcctgatag	tcagcatatt	gcgatacctgg	360
aatgagcctc	tgtatcatct	ggtcacggaa	gtacgtggta	tgcaagaagc	cccggagggt	420
atcctatcca	aagctgtaga	gattgaggag	caaaccaaac	ggcttctaga	gggcatggag	480
ctgatagtca	gccaggttca	tcctgaaacc	aaagaaaatg	agatctaccc	tgtctggtcg	540
ggactttccat	ccctgcagat	ggctgatgaa	gagctctgcc	tttctgctta	ttataacctg	600
ctccactgcc	tacgcaggga	tnnncataaa	atcgacaatt	atctcaagct	cctgaagtgc	660
cgaatcatcc	acaacaacaa	ctgctaagcc	cacatccatt	tcatactatt	ctgagaaggt	720
ccttaatgat	ccgttccatt	gcaagcttct	tttagttgta	tctcttttga	atccatgctt	780
gggtgtaaca	ggtctcctct	taaaaaataa	aaactgactc	gttagagaca	tc	832

<210> 2

<211> 228

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> 208

<223> Site mutated amino acid residue where the normal
codon coding for serine is modified preferably to encode
for aspartate or glutamate, most preferably
aspartate.

<400> 2

Asn Met Asn Ile Lys Gly Ser Pro Trp Lys Gly Ser Leu Leu Leu Leu
 1 5 10 15
 Leu Val Ser Asn Leu Leu Cys Gln Ser Val Ala Pro Leu Pro Ile
 20 25 30
 Cys Pro Gly Gly Ala Ala Arg Cys Gln Val Thr Leu Arg Asp Leu Phe
 35 40 45
 Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn Leu Ser Ser Glu
 50 55 60
 Met Phe Ser Glu Phe Asp Lys Arg Tyr Thr His Gly Arg Gly Phe Ile
 65 70 75 80
 Thr Lys Ala Ile Asn Ser Cys His Thr Ser Ser Leu Ala Thr Pro Glu
 85 90 95
 Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp Phe Leu Ser Leu
 100 105 110
 Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu Tyr His Leu Val
 115 120 125
 Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala Ile Leu Ser Lys
 130 135 140
 Ala Val Glu Ile Glu Glu Gln Thr Lys Arg Leu Glu Gly Met Glu
 145 150 155 160
 Leu Ile Val Ser Gln Val His Pro Glu Thr Lys Glu Asn Glu Ile Tyr
 165 170 175
 Pro Val Trp Ser Gly Leu Pro Ser Leu Gln Met Ala Asp Glu Glu Ser
 180 185 190
 Arg Leu Ser Ala Tyr Tyr Asn Leu Leu His Cys Leu Arg Arg Asp Xaa
 195 200 205
 His Lys Ile Asp Asn Tyr Leu Lys Leu Leu Lys Cys Arg Ile Ile His
 210 215 220
 Asn Asn Asn Cys
 225

<210> 3

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> This sequence is a primer.

<400> 3

gcagggatga ccacaagggtt gac

23

<210> 4

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> This sequence is a primer.

<220>

<221> variation

<222> 12

<223> This is a nucleic acid residue that can be replaced for nucleic acid substitutes.

<400> 4

cgcaagggtt gnacacaagg ttga

24

<210> 5

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> This sequence is a primer.

<220>

<221> variation

<222> 12

<223> This is a nucleic acid residue that can be replaced for nucleic acid substitutes.

<400> 5

acgcagggat gnkataaaat cg

22

<210> 6

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> This sequence is a primer.

<400> 6

cgtggccccc atatgttgcc catctg

26